

SEQUENCE LISTING

<110> Gorman, Daniel M.

<120> MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS

<130> DX01170K1

<150> US 60/206,862

<151> 2000-05-24

<160> 24

<170> PatentIn version 3.2

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cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac	144
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Val Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn	
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Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
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Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
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Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
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 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
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Pro Gln Ile Ile Thr Leu Asn His Thr Asp Leu Val Pro Cys Leu Cys	
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Pro Phe Arg Glu Asp Pro Arg Ala His Gln Asn Leu Trp Gln Ala Ala	
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Asp Leu Cys Leu Arg Val Ala Val His Leu Ala Val His Gly His Trp
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Val Glu Glu Pro Arg Asn Ala Ser Leu Gln Ala Gln Val Val Leu Ser
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290

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Asp Ser Leu Gly Pro Leu Lys Asp Asp Val Leu Leu Leu Glu Thr Arg
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Thr Lys Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu	
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			640				645						650				
tcc	gag	ctg	tct	ctg	cca	ctg	atg	gaa	gga	ctc	tcg	acg	gac	cag	aca	2127	
Ser	Glu	Leu	Ser	Leu	Pro	Leu	Met	Glu	Gly	Leu	Ser	Thr	Asp	Gln	Thr		
			655				660						665			670	
gaa	acg	tct	tcc	ctg	acg	gag	agc	gtg	tcc	tcc	tct	tca	ggc	ctg	ggc	2175	
Glu	Thr	Ser	Ser	Leu	Thr	Glu	Ser	Val	Ser	Ser	Ser	Ser	Gly	Leu	Gly		
			675							680			685				
gag	gag	gaa	cct	cct	gcc	ctt	cct	tcc	aag	ctc	ctc	tct	tct	ggg	tca	2223	
Glu	Glu	Glu	Pro	Pro	Ala	Leu	Pro	Ser	Lys	Leu	Leu	Ser	Ser	Gly	Ser		
			690				695						700				
tgc	aaa	gca	gat	ctt	ggc	tgc	cgc	agc	tac	act	gat	gaa	ctc	cac	gcg	2271	
Cys	Lys	Ala	Asp	Leu	Gly	Cys	Arg	Ser	Tyr	Thr	Asp	Glu	Leu	His	Ala		
			705				710						715				
gtc	gcc	cct	ttg	taacaaaacg			aaagagtcta			agcattgcc			ctttagctgc			2323	
Val	Ala	Pro	Leu														
			720														
tgctccctc tgattcccca gctcatctcc ctggttgcat ggcccacttg gagctgaggt																2383	
ctcatacaag gatatttgga gtgaaatgct ggccagtact tgttctccct tgccccaacc																2443	
ctttaccgga tatcttgaca aactctccaa ttttctaaaa tgatatggag ctctgaaagg																	

cagacttcat tgagctctgc aaactttgcc tgtttgctat tggctacctt gatttgaaat 2683
gctttgtgaa aaaaggcact tttaacatca tagccacaga aatcaagtgc cagtctatct 2743
ggaatccatg ttgtattgca gataatgttc tcatttattt ttg 2786

<210> 10
<211> 738
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (18)..(18)
<223> The 'Xaa' at location 18 stands for Gln, Arg, Pro, or Leu.

<220>
<221> misc_feature
<222> (26)..(26)
<223> The 'Xaa' at location 26 stands for Lys, Arg, Thr, or Met.

<220>
<221> misc_feature
<222> (109)..(109)
<223> The 'Xaa' at location 109 stands for Ser, Gly, Arg, or Cys.

<220>
<221> misc_feature
<222> (120)..(120)
<223> The 'Xaa' at location 120 stands for Ile, Val, Leu, or Phe.

<220>
<221> misc_feature
<222> (134)..(134)
<223> The 'Xaa' at location 134 stands for Leu, or Phe.

<400> 10

Met Ala Pro Trp Leu Gln Leu Cys Ser Val Phe Phe Thr Val Asn Ala
-15 -10 -5 -1

Cys Leu Asn Gly Ser Gln Leu Ala Val Ala Ala Gly Gly Ser Gly Arg
1 5 10 15

Ala Xaa Gly Ala Asp Thr Cys Ser Trp Xaa Gly Val Gly Pro Ala Ser
20 25 30

Arg Asn Ser Gly Leu Tyr Asn Ile Thr Phe Lys Tyr Asp Asn Cys Thr
35 40 45

Thr Tyr Leu Asn Pro Val Gly Lys His Val Ile Ala Asp Ala Gln Asn
50 55 60

Ile Thr Ile Ser Gln Tyr Ala Cys His Asp Gln Val Ala Val Thr Ile
65 70 75 80

Leu Trp Ser Pro Gly Ala Leu Gly Ile Glu Phe Leu Lys Gly Phe Arg
85 90 95

Val Ile Leu Glu Glu Leu Lys Ser Glu Gly Arg Gln Xaa Gln Gln Leu
100 105 110

Ile Leu Lys Asp Pro Lys Gln Xaa Asn Ser Ser Phe Lys Arg Thr Gly
115 120 125

Met Glu Ser Gln Pro Xaa Leu Asn Met Lys Phe Glu Thr Asp Tyr Phe
130 135 140

Val Arg Leu Ser Phe Ser Phe Ile Lys Asn Glu Ser Asn Tyr His Pro
145 150 155 160

Phe Phe Phe Arg Thr Arg Ala Cys Asp Leu Leu Leu Gln Pro Asp Asn
165 170 175

Leu Ala Cys Lys Pro Phe Trp Lys Pro Arg Asn Leu Asn Ile Ser Gln
180 185 190

His Gly Ser Asp Met Gln Val Ser Phe Asp His Ala Pro His Asn Phe
195 200 205

Gly Phe Arg Phe Phe Tyr Leu His Tyr Lys Leu Lys His Glu Gly Pro
210 215 220

Phe Lys Arg Lys Thr Cys Lys Gln Glu Gln Thr Thr Glu Met Thr Ser
225 230 235 240

Cys Leu Leu Gln Asn Val Ser Pro Gly Asp Tyr Ile Ile Glu Leu Val
245 250 255

Asp Asp Thr Asn Thr Thr Arg Lys Val Met His Tyr Ala Leu Lys Pro
260 265 270

Val His Ser Pro Trp Ala Gly Pro Ile Arg Ala Val Ala Ile Thr Val
275 280 285

Pro Leu Val Val Ile Ser Ala Phe Ala Thr Leu Phe Thr Val Met Cys
290 295 300

Arg Lys Lys Gln Gln Glu Asn Ile Tyr Ser His Leu Asp Glu Glu Ser
305 310 315 320

Ser Glu Ser Ser Thr Tyr Thr Ala Ala Leu Pro Arg Glu Arg Leu Arg
325 330 335

Pro Arg Pro Lys Val Phe Leu Cys Tyr Ser Ser Lys Asp Gly Gln Asn
340 345 350

His Met Asn Val Val Gln Cys Phe Ala Tyr Phe Leu Gln Asp Phe Cys
355 360 365

Gly Cys Glu Val Ala Leu Asp Leu Trp Glu Asp Phe Ser Leu Cys Arg
370 375 380

Glu Gly Gln Arg Glu Trp Val Ile Gln Lys Ile His Glu Ser Gln Phe
385 390 395 400

Ile Ile Val Val Cys Ser Lys Gly Met Lys Tyr Phe Val Asp Lys Lys
405 410 415

Asn Tyr Lys His Lys Gly Gly Gly Arg Gly Ser Gly Lys Gly Glu Leu
420 425 430

Phe Leu Val Ala Val Ser Ala Ile Ala Glu Lys Leu Arg Gln Ala Lys
435 440 445

Gln Ser Ser Ser Ala Ala Leu Ser Lys Phe Ile Ala Val Tyr Phe Asp
450 455 460

Tyr Ser Cys Glu Gly Asp Val Pro Gly Ile Leu Asp Leu Ser Thr Lys
465 470 475 480

Tyr Arg Leu Met Asp Asn Leu Pro Gln Leu Cys Ser His Leu His Ser
485 490 495

Arg Asp His Gly Leu Gln Glu Pro Gly Gln His Thr Arg Gln Gly Ser
500 505 510

Arg Arg Asn Tyr Phe Arg Ser Lys Ser Gly Arg Ser Leu Tyr Val Ala
515 520 525

Ile Cys Asn Met His Gln Phe Ile Asp Glu Glu Pro Asp Trp Phe Glu
530 535 540

Lys Gln Phe Val Pro Phe His Pro Pro Pro Leu Arg Tyr Arg Glu Pro
545 550 555 560

Val Leu Glu Lys Phe Asp Ser Gly Leu Val Leu Asn Asp Val Met Cys
565 570 575

Lys Pro Gly Pro Glu Ser Asp Phe Cys Leu Lys Val Glu Ala Ala Val
580 585 590

Leu Gly Ala Thr Gly Pro Ala Asp Ser Gln His Glu Ser Gln His Gly
595 600 605

Gly Leu Asp Gln Asp Gly Glu Ala Arg Pro Ala Leu Asp Gly Ser Ala
610 615 620

Ala Leu Gln Pro Leu Leu His Thr Val Lys Ala Gly Ser Pro Ser Asp
625 630 635 640

Met Pro Arg Asp Ser Gly Ile Tyr Asp Ser Ser Val Pro Ser Ser Glu
645 650 655

Leu Ser Leu Pro Leu Met Glu Gly Leu Ser Thr Asp Gln Thr Glu Thr
660 665 670

Ser Ser Leu Thr Glu Ser Val Ser Ser Ser Ser Gly Leu Gly Glu Glu
675 680 685

Glu Pro Pro Ala Leu Pro Ser Lys Leu Leu Ser Ser Gly Ser Cys Lys
690 695 700

Ala Asp Leu Gly Cys Arg Ser Tyr Thr Asp Glu Leu His Ala Val Ala
705 710 715 720

Pro Leu

<210> 11
<211> 2012
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)..(1971)

<220>
<221> mat_peptide
<222> (70)..()

<400> 11
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Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile

	-20		-15		-10		
	gtc atc gac ctc tct gac tct gct ggg att ggc ttt cgc cac ctg ccc					96	
	Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro						
	-5		-1 1		5		
	cac tgg aac acc cgc tgt cct ctg gcc tcc cac acg gaa gtt ctg cct					144	
	His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro						
	10		15		20		25
	ata tcc ctt gcc gca cct ggt ggg ccc tct tct cca caa agc ctt ggt					192	
	Ile Ser Leu Ala Ala Pro Gly Gly Pro Ser Ser Pro Gln Ser Leu Gly						
		30		35			40
	gtg tgc gag tct ggc act gtt ccc gct gtt tgt gcc agc atc tgc tgt					240	
	Val Cys Glu Ser Gly Thr Val Pro Ala Val Cys Ala Ser Ile Cys Cys						
		45		50			55
	cag gtg gct cag gtc ttc aac ggg gcc tct tcc acc tcc tgg tgc aga					288	
	Gln Val Ala Gln Val Phe Asn Gly Ala Ser Ser Thr Ser Trp Cys Arg						
		60		65			70
	aat cca aaa agt ctt cca cat tca agt tct ata gga gac aca aga tgc					336	
	Asn Pro Lys Ser Leu Pro His Ser Ser Ser Ile Gly Asp Thr Arg Cys						
		75		80			85
	cag cac ctg ctc aga gga agc tgc tgc ctc gtc gtc acc tgt ctg aga					384	
	Gln His Leu Leu Arg Gly Ser Cys Cys Leu Val Val Thr Cys Leu Arg						
		90		95			100
	aga gcc atc aca ttt cca tcc cct ccc cag aca tct ccc aca agg gac					432	
	Arg Ala Ile Thr Phe Pro Ser Pro Pro Gln Thr Ser Pro Thr Arg Asp						
		110		115			120
	ttc gct cta aaa gga ccc aac ctt cgg atc cag aga cat ggg aaa gtc					480	
	Phe Ala Leu Lys Gly Pro Asn Leu Arg Ile Gln Arg His Gly Lys Val						
		125		130			135
	ttc cca gat tgg act cac aaa ggc atg gag gtg ggc act ggg tac aac					528	
	Phe Pro Asp Trp Thr His Lys Gly Met Glu Val Gly Thr Gly Tyr Asn						
		140		145			150
	agg aga tgg gtt cag ctg agt ggt gga ccc gag ttc tcc ttt gat ttg					576	
	Arg Arg Trp Val Gln Leu Ser Gly Gly Pro Glu Phe Ser Phe Asp Leu						
		155		160			165
	ctg cct gag gcc cgg gct att cgg gtg acc ata tct tca ggc cct gag					624	
	Leu Pro Glu Ala Arg Ala Ile Arg Val Thr Ile Ser Ser Gly Pro Glu						
		170		175			180
	gtc agc gtg cgt ctt tgt cac cag tgg gca ctg gag tgt gaa gag ctg					672	
	Val Ser Val Arg Leu Cys His Gln Trp Ala Leu Glu Cys Glu Glu Leu						
		190		195			200
	agc agt ccc tat gat gtc cag aaa att gtg tct ggg ggc cac act gta					720	
	Ser Ser Pro Tyr Asp Val Gln Lys Ile Val Ser Gly Gly His Thr Val						
		205		210			215
	gag ctg cct tat gaa ttc ctt ctg ccc tgt ctg tgc ata gag gca tcc					768	
	Glu Leu Pro Tyr Glu Phe Leu Leu Pro Cys Leu Cys Ile Glu Ala Ser						
		220		225			230

tac ctg caa gag gac act gtg agg cgc aaa aaa tgt ccc ttc cag agc Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Lys Cys Pro Phe Gln Ser 235 240 245	816
tgg cca gaa gcc tat ggc tcg gac ttc tgg aag tca gtg cac ttc act Trp Pro Glu Ala Tyr Gly Ser Asp Phe Trp Lys Ser Val His Phe Thr 250 255 260 265	864
gac tac agc cag cac act cag atg gtc atg gcc ctg aca ctc cgc tgc Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys 270 275 280	912
cca ctg aag ctg gaa gct gcc ctc tgc cag agg cac gac tgg cat acc Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr 285 290 295	960
ctt tgc aaa gac ctc ccg aat gcc acg gct cga gag tca gat ggg tgg Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp 300 305 310	1008
tat gtt ttg gag aag gtg gac ctg cac ccc cag ctc tgc ttc aag gta Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val 315 320 325	1056
caa cca tgg ttc tct ttt gga aac agc agc cat gtt gaa tgc ccc cac Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His 330 335 340 345	1104
cag act ggg tct ctc aca tcc tgg aat gta agc atg gat acc caa gcc Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala 350 355 360	1152
cag cag ctg att ctt cac ttc tcc tca aga atg cat gcc acc ttc agt Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser 365 370 375	1200
gct gcc tgg agc ctc cca ggc ttg ggg cag gac act ttg gtg ccc ccc Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro 380 385 390	1248
gtg tac act gtc agc cag gtg tgg cgg tca gat gtc cag ttt gcc tgg Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp 395 400 405	1296
aag cac ctc ttg tgt cca gat gtc tct tac aga cac ctg ggg ctc ttg Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu 410 415 420 425	1344
atc ctg gca ctg ctg gcc ctc ctc acc cta ctg ggt gtt gtt ctg gcc Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala 430 435 440	1392
ctc acc tgc cgg cgc cca cag tca ggc ccg ggc cca gcg cgg cca gtg Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val 445 450 455	1440
ctc ctc ctg cac gcg gcg gac tcg gag gcg cag cgg cgc ctg gtg gga Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly 460 465 470	1488

gcg ctg gct gaa ctg cta cgg gca gcg ctg ggc ggc ggg cgc gac gtg Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val 475 480 485	1536
atc gtg gac ctg tgg gag ggg agg cac gtg gcg cgc gtg ggc ccg ctg Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu 490 495 500 505	1584
ccg tgg ctc tgg gcg gcg cgg acg cgc gta gcg cgg gag cag ggc act Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr 510 515 520	1632
gtg ctg ctg ctg tgg agc ggc gcc gac ctt cgc ccg gtc agc ggc ccc Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro 525 530 535	1680
gac ccc cgc gcc gcg ccc ctg ctc gcc ctg ctc cac gct gcc ccg cgc Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg 540 545 550	1728
ccg ctg ctg ctg ctc gct tac ttc agt cgc ctc tgc gcc aag ggc gac Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp 555 560 565	1776
atc ccc ccg ccg ctg cgc gcc ctg ccg cgc tac cgc ctg ctg cgc gac Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp 570 575 580 585	1824
ctg ccg cgt ctg ctg cgg gcg ctg gac gcg cgg cct ttc gca gag gcc Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala 590 595 600	1872
acc agc tgg ggc cgc ctt ggg gcg cgg cag cgc agg cag agc cgc cta Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu 605 610 615	1920
gag ctg tgc agc cgg ctc gaa cga gag gcc gcc cga ctt gca gac cta Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu 620 625 630	1968
ggt tgagcagagc tccaccgcag tcccgggtgt ctgcggccgc t Gly	2012

<210> 12
 <211> 657
 <212> PRT
 <213> Homo sapiens

<400> 12

Met Gly Ser Ser Arg Leu Ala Ala Leu Leu Leu Pro Leu Leu Leu Ile	
-20	-15 -10

Val Ile Asp Leu Ser Asp Ser Ala Gly Ile Gly Phe Arg His Leu Pro	
-5 -1 1 5	

His Trp Asn Thr Arg Cys Pro Leu Ala Ser His Thr Glu Val Leu Pro

10	15	20	25
Ile Ser Leu Ala	Ala Pro Gly Gly	Pro Ser Ser Pro	Gln Ser Leu Gly
	30	35	40
Val Cys Glu Ser	Gly Thr Val Pro	Ala Val Cys Ala	Ser Ile Cys Cys
	45	50	55
Gln Val Ala Gln	Val Phe Asn Gly	Ala Ser Ser Thr	Ser Trp Cys Arg
	60	65	70
Asn Pro Lys Ser	Leu Pro His Ser	Ser Ser Ser Ile	Gly Asp Thr Arg Cys
	75	80	85
Gln His Leu Leu	Arg Gly Ser Cys	Cys Leu Val Val	Thr Cys Leu Arg
	90	95	100
Arg Ala Ile Thr	Phe Pro Ser Pro	Pro Gln Thr Ser	Pro Thr Arg Asp
	110	115	120
Phe Ala Leu Lys	Gly Pro Asn Leu	Arg Ile Gln Arg	His Gly Lys Val
	125	130	135
Phe Pro Asp Trp	Thr His Lys Gly	Met Glu Val Gly	Thr Gly Tyr Asn
	140	145	150
Arg Arg Trp Val	Gln Leu Ser Gly	Gly Pro Glu Phe	Ser Phe Asp Leu
	155	160	165
Leu Pro Glu Ala	Arg Ala Ile Arg	Val Thr Ile Ser	Ser Gly Pro Glu
	170	175	180
Val Ser Val Arg	Leu Cys His Gln	Trp Ala Leu Glu	Cys Glu Glu Leu
	190	195	200
Ser Ser Pro Tyr	Asp Val Gln Lys	Ile Val Ser Gly	Gly His Thr Val
	205	210	215
Glu Leu Pro Tyr	Glu Phe Leu Leu	Pro Cys Leu Cys	Ile Glu Ala Ser
	220	225	230
Tyr Leu Gln Glu	Asp Thr Val Arg	Arg Lys Lys Cys	Pro Phe Gln Ser
	235	240	245
Trp Pro Glu Ala	Tyr Gly Ser Asp	Phe Trp Lys Ser	Val His Phe Thr
	250	255	260
			265

Asp Tyr Ser Gln His Thr Gln Met Val Met Ala Leu Thr Leu Arg Cys
270 275 280

Pro Leu Lys Leu Glu Ala Ala Leu Cys Gln Arg His Asp Trp His Thr
285 290 295

Leu Cys Lys Asp Leu Pro Asn Ala Thr Ala Arg Glu Ser Asp Gly Trp
300 305 310

Tyr Val Leu Glu Lys Val Asp Leu His Pro Gln Leu Cys Phe Lys Val
315 320 325

Gln Pro Trp Phe Ser Phe Gly Asn Ser Ser His Val Glu Cys Pro His
330 335 340 345

Gln Thr Gly Ser Leu Thr Ser Trp Asn Val Ser Met Asp Thr Gln Ala
350 355 360

Gln Gln Leu Ile Leu His Phe Ser Ser Arg Met His Ala Thr Phe Ser
365 370 375

Ala Ala Trp Ser Leu Pro Gly Leu Gly Gln Asp Thr Leu Val Pro Pro
380 385 390

Val Tyr Thr Val Ser Gln Val Trp Arg Ser Asp Val Gln Phe Ala Trp
395 400 405

Lys His Leu Leu Cys Pro Asp Val Ser Tyr Arg His Leu Gly Leu Leu
410 415 420 425

Ile Leu Ala Leu Leu Ala Leu Leu Thr Leu Leu Gly Val Val Leu Ala
430 435 440

Leu Thr Cys Arg Arg Pro Gln Ser Gly Pro Gly Pro Ala Arg Pro Val
445 450 455

Leu Leu Leu His Ala Ala Asp Ser Glu Ala Gln Arg Arg Leu Val Gly
460 465 470

Ala Leu Ala Glu Leu Leu Arg Ala Ala Leu Gly Gly Gly Arg Asp Val
475 480 485

Ile Val Asp Leu Trp Glu Gly Arg His Val Ala Arg Val Gly Pro Leu
490 495 500 505

Pro Trp Leu Trp Ala Ala Arg Thr Arg Val Ala Arg Glu Gln Gly Thr
510 515 520

Val Leu Leu Leu Trp Ser Gly Ala Asp Leu Arg Pro Val Ser Gly Pro
525 530 535

Asp Pro Arg Ala Ala Pro Leu Leu Ala Leu Leu His Ala Ala Pro Arg
540 545 550

Pro Leu Leu Leu Leu Ala Tyr Phe Ser Arg Leu Cys Ala Lys Gly Asp
555 560 565

Ile Pro Pro Pro Leu Arg Ala Leu Pro Arg Tyr Arg Leu Leu Arg Asp
570 575 580 585

Leu Pro Arg Leu Leu Arg Ala Leu Asp Ala Arg Pro Phe Ala Glu Ala
590 595 600

Thr Ser Trp Gly Arg Leu Gly Ala Arg Gln Arg Arg Gln Ser Arg Leu
605 610 615

Glu Leu Cys Ser Arg Leu Glu Arg Glu Ala Ala Arg Leu Ala Asp Leu
620 625 630

Gly

<210> 13
<211> 808
<212> DNA
<213> Mus musculus

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<221> CDS
<222> (78)..(806)

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<221> mat_peptide
<222> (147)..()

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tgatcctaca gaagctc atg ggg agc ccc aga ctg gca gcc ttg ctc ctg 110
Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu
-20 -15

tct ctc ccg cta ctg ctc atc ggc ctc gct gtg tct gct cgg gtt gcc 158
Ser Leu Pro Leu Leu Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala
-10 -5 -1 1

tgc ccc tgc ctg cgg agt tgg acc agc cac tgt ctc ctg gcc tac cgt Cys Pro Cys Leu Arg Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg 5 10 15 20	206
gtg gat aaa cgt ttt gct ggc ctt cag tgg ggc tgg ttc cct ctc ttg Val Asp Lys Arg Phe Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu 25 30 35	254
gtg agg aaa tct aaa agt cct cct aaa ttt gaa gac tat tgg agg cac Val Arg Lys Ser Lys Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His 40 45 50	302
agg aca cca gca tcc ttc cag agg aag ctg cta ggc agc cct tcc ctg Arg Thr Pro Ala Ser Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu 55 60 65	350
tct gag gaa agc cat cga att tcc atc ccc tcc tca gcc atc tcc cac Ser Glu Glu Ser His Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His 70 75 80	398
aga ggc caa cgc acc aaa agg gcc cag cct tca gct gca gaa gga aga Arg Gly Gln Arg Thr Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg 85 90 95 100	446
gaa cat ctc cct gaa gca ggg tca caa aag tgt gga gga cct gaa ttc Glu His Leu Pro Glu Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe 105 110 115	494
tcc ttt gat ttg ctg ccc gag gtg cag gct gtt cgg gtg act att cct Ser Phe Asp Leu Leu Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro 120 125 130	542
gca ggc ccc aag gca cgt gtg cgc ctt tgt tat cag tgg gca ctg gaa Ala Gly Pro Lys Ala Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu 135 140 145	590
tgt gaa gac ttg agt agc cct ttt gat acc cag aaa att gtg tct gga Cys Glu Asp Leu Ser Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly 150 155 160	638
ggg cac act gta gac ctg cct tat gaa ttc ctt ctg ccc tgc atg tgc Gly His Thr Val Asp Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys 165 170 175 180	686
ata gag gcc tcc tac ctg caa gag gac act gtg agg cgc aaa agt gtc Ile Glu Ala Ser Tyr Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val 185 190 195	734
cct tcc aga gct ggc ctg aag ctt atg gct cag act tct ggc agt caa Pro Ser Arg Ala Gly Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln 200 205 210	782
tac gct tca ctg act aca gcc agc ac Tyr Ala Ser Leu Thr Thr Ala Ser 215 220	808

<210> 14
 <211> 243
 <212> PRT

<213> Mus musculus

<400> 14

Met Gly Ser Pro Arg Leu Ala Ala Leu Leu Leu Ser Leu Pro Leu Leu
-20 -15 -10

Leu Ile Gly Leu Ala Val Ser Ala Arg Val Ala Cys Pro Cys Leu Arg
-5 -1 1 5

Ser Trp Thr Ser His Cys Leu Leu Ala Tyr Arg Val Asp Lys Arg Phe
10 15 20 25

Ala Gly Leu Gln Trp Gly Trp Phe Pro Leu Leu Val Arg Lys Ser Lys
30 35 40

Ser Pro Pro Lys Phe Glu Asp Tyr Trp Arg His Arg Thr Pro Ala Ser
45 50 55

Phe Gln Arg Lys Leu Leu Gly Ser Pro Ser Leu Ser Glu Glu Ser His
60 65 70

Arg Ile Ser Ile Pro Ser Ser Ala Ile Ser His Arg Gly Gln Arg Thr
75 80 85

Lys Arg Ala Gln Pro Ser Ala Ala Glu Gly Arg Glu His Leu Pro Glu
90 95 100 105

Ala Gly Ser Gln Lys Cys Gly Gly Pro Glu Phe Ser Phe Asp Leu Leu
110 115 120

Pro Glu Val Gln Ala Val Arg Val Thr Ile Pro Ala Gly Pro Lys Ala
125 130 135

Arg Val Arg Leu Cys Tyr Gln Trp Ala Leu Glu Cys Glu Asp Leu Ser
140 145 150

Ser Pro Phe Asp Thr Gln Lys Ile Val Ser Gly Gly His Thr Val Asp
155 160 165

Leu Pro Tyr Glu Phe Leu Leu Pro Cys Met Cys Ile Glu Ala Ser Tyr
170 175 180 185

Leu Gln Glu Asp Thr Val Arg Arg Lys Ser Val Pro Ser Arg Ala Gly
190 195 200

Leu Lys Leu Met Ala Gln Thr Ser Gly Ser Gln Tyr Ala Ser Leu Thr

205

210

215

Thr Ala Ser
220

<210> 15
<211> 2377
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (180)..(1874)

<400> 15
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cagagcctgt tcttctactt acctgggccc ggagaagggtg gagggagacg agaagccgcc 120
gagagccgac taccctccgg gccagctctg tctgtccgtg gtggatctaa gaaactaga 179
atg aac cga agc att cct gtg gag gtt gat gaa tca gaa cca tac cca 227
Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
1 5 10 15
agt cag ttg ctg aaa cca atc cca gaa tat tcc ccg gaa gag gaa tca 275
Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
20 25 30
gaa cca cct gct cca aat ata agg aac atg gca ccc aac agc ttg tct 323
Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
35 40 45
gca ccc aca atg ctt cac aat tcc tcc gga gac ttt tct caa gct cac 371
Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
50 55 60
tca acc ctg aaa ctt gca aat cac cag cgg cct gta tcc cgg cag gtc 419
Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
65 70 75 80
acc tgc ctg cgc act caa gtt ctg gag gac agt gaa gac agt ttc tgc 467
Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys
85 90 95
agg aga cac cca ggc ctg ggc aaa gct ttc cct tct ggg tgc tct gca 515
Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala
100 105 110
gtc agc gag cct gcg tct gag tct gtg gtt gga gcc ctc cct gca gag 563
Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu
115 120 125
cat cag ttt tca ttt atg gaa aaa cgt aat caa tgg ctg gta tct cag 611
His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln
130 135 140
ctt tca gcg gct tct cct gac act ggc cat gac tca gac aaa tca gac 659

Leu	Ser	Ala	Ala	Ser	Pro	Asp	Thr	Gly	His	Asp	Ser	Asp	Lys	Ser	Asp		
145					150					155					160		
caa	agt	tta	cct	aat	gcc	tca	gca	gac	tcc	ttg	ggc	ggt	agc	cag	gag	707	
Gln	Ser	Leu	Pro	Asn	Ala	Ser	Ala	Asp	Ser	Leu	Gly	Gly	Ser	Gln	Glu		
				165					170					175			
atg	gtg	caa	cgg	ccc	cag	cct	cac	agg	aac	cga	gca	ggc	ctg	gat	ctg	755	
Met	Val	Gln	Arg	Pro	Gln	Pro	His	Arg	Asn	Arg	Ala	Gly	Leu	Asp	Leu		
			180					185					190				
cca	acc	ata	gac	acg	gga	tat	gat	tcc	cag	ccc	cag	gat	gtc	ctg	ggc	803	
Pro	Thr	Ile	Asp	Thr	Gly	Tyr	Asp	Ser	Gln	Pro	Gln	Asp	Val	Leu	Gly		
		195					200					205					
atc	agg	cag	ctg	gaa	agg	ccc	ctg	ccc	ctc	acc	tcc	gtg	tgt	tac	ccc	851	
Ile	Arg	Gln	Leu	Glu	Arg	Pro	Leu	Pro	Leu	Thr	Ser	Val	Cys	Tyr	Pro		
	210					215					220						
cag	gac	ctc	ccc	aga	cct	ctc	agg	tcc	agg	gag	ttc	cct	cag	ttt	gaa	899	
Gln	Asp	Leu	Pro	Arg	Pro	Leu	Arg	Ser	Arg	Glu	Phe	Pro	Gln	Phe	Glu		
225					230					235					240		
cct	cag	agg	tat	cca	gca	tgt	gca	cag	atg	ctg	cct	ccc	aat	ctt	tcc	947	
Pro	Gln	Arg	Tyr	Pro	Ala	Cys	Ala	Gln	Met	Leu	Pro	Pro	Asn	Leu	Ser		
				245					250					255			
cca	cat	gct	cca	tgg	aac	tat	cat	tac	cat	tgt	cct	gga	agt	ccc	gat	995	
Pro	His	Ala	Pro	Trp	Asn	Tyr	His	Tyr	His	Cys	Pro	Gly	Ser	Pro	Asp		
			260					265					270				
cac	cag	gtg	cca	tat	ggc	cat	gac	tac	cct	cga	gca	gcc	tac	cag	caa	1043	
His	Gln	Val	Pro	Tyr	Gly	His	Asp	Tyr	Pro	Arg	Ala	Ala	Tyr	Gln	Gln		
		275					280					285					
gtg	atc	cag	ccg	gct	ctg	cct	ggg	cag	ccc	ctg	cct	gga	gcc	agt	gtg	1091	
Val	Ile	Gln	Pro	Ala	Leu	Pro	Gly	Gln	Pro	Leu	Pro	Gly	Ala	Ser	Val		
	290					295					300						
aga	ggc	ctg	cac	cct	gtg	cag	aag	gtt	atc	ctg	aat	tat	ccc	agc	ccc	1139	
Arg	Gly	Leu	His	Pro	Val	Gln	Lys	Val	Ile	Leu	Asn	Tyr	Pro	Ser	Pro		
305					310					315					320		
tgg	gac	caa	gaa	gag	agg	ccc	gca	cag	aga	gac	tgc	tcc	ttt	ccg	ggg	1187	
Trp	Asp	Gln	Glu	Glu	Arg	Pro	Ala	Gln	Arg	Asp	Cys	Ser	Phe	Pro	Gly		
				325					330					335			
ctt	cca	agg	cac	cag	gac	cag	cca	cat	cac	cag	cca	cct	aat	aga	gct	1235	
Leu	Pro	Arg	His	Gln	Asp	Gln	Pro	His	His	Gln	Pro	Pro	Asn	Arg	Ala		
			340					345					350				
ggg	gct	cct	ggg	gag	tcc	ttg	gag	tgc	cct	gca	gag	ctg	aga	cca	cag	1283	
Gly	Ala	Pro	Gly	Glu	Ser	Leu	Glu	Cys	Pro	Ala	Glu	Leu	Arg	Pro	Gln		
		355					360					365					
gtt	ccc	cag	cct	ccg	tcc	cca	gct	gct	gtg	cct	aga	ccc	cct	agc	aac	1331	
Val	Pro	Gln	Pro	Pro	Ser	Pro	Ala	Ala	Val	Pro	Arg	Pro	Pro	Ser	Asn		
		370				375					380						
cct	cca	gcc	aga	gga	act	cta	aaa	aca	agc	aat	ttg	cca	gaa	gaa	ttg	1379	
Pro	Pro	Ala	Arg	Gly	Thr	Leu	Lys	Thr	Ser	Asn	Leu	Pro	Glu	Glu	Leu		

385	390	395	400	
cgg aaa gtc ttt atc act tat tcg atg gac aca gct atg gag gtg gtg				1427
Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val				
	405	410	415	
aaa ttc gtg aac ttt ttg ttg gta aat ggc ttc caa act gca att gac				1475
Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp				
	420	425	430	
ata ttt gag gat aga atc cga ggc att gat atc att aaa tgg atg gag				1523
Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu				
	435	440	445	
cgc tac ctt agg gat aag acc gtg atg ata atc gta gca atc agc ccc				1571
Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro				
	450	455	460	
aaa tac aaa cag gac gtg gaa ggc gct gag tcg cag ctg gac gag gat				1619
Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp				
	465	470	475	480
gag cat ggc tta cat act aag tac att cat cga atg atg cag att gag				1667
Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu				
	485	490	495	
ttc ata aaa caa gga agc atg aat ttc aga ttc atc cct gtg ctc ttc				1715
Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe				
	500	505	510	
cca aat gct aag aag gag cat gtg ccc acc tgg ctt cag aac act cat				1763
Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His				
	515	520	525	
gtc tac agc tgg ccc aag aat aaa aaa aac atc ctg ctg cgg ctg ctg				1811
Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu				
	530	535	540	
aga gag gaa gag tat gtg gct cct cca cgg ggg cct ctg ccc acc ctt				1859
Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu				
	545	550	555	560
cag gtg gtt ccc ttg tgacaccgtt catccccaga tcaactgaggc caggccatgt				1914
Gln Val Val Pro Leu				
	565			
ttggggcctt gttctgacag cattctggct gaggctggtc ggtagcactc ctggctgggt				1974
tttttctggt cctccccgag aggcctctct gccccagga aacctgttgt gcagagctct				2034
tccccggaga cctccacaca cctggcttt gaagtggagt ctgtgactgc tctgcattct				2094
ctgcttttaa aaaaaccatt gcaggtgcca gtgtcccata tgttcctcct gacagtttga				2154
tgtgtccatt ctgggcctct cagtgttag caagtagata atgtaaggga tgtggcagca				2214
aatggaaatg actacaaaca ctctcctatc aatcacttca ggctactttt atgagtttagc				2274
cagatgcttg tgtatcctca gaccaaactg attcatgtac aaataataaa atgtttactc				2334
ttttgtaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa				2377

<210> 16
<211> 565
<212> PRT
<213> Homo sapiens

<400> 16

Met Asn Arg Ser Ile Pro Val Glu Val Asp Glu Ser Glu Pro Tyr Pro
1 5 10 15

Ser Gln Leu Leu Lys Pro Ile Pro Glu Tyr Ser Pro Glu Glu Glu Ser
20 25 30

Glu Pro Pro Ala Pro Asn Ile Arg Asn Met Ala Pro Asn Ser Leu Ser
35 40 45

Ala Pro Thr Met Leu His Asn Ser Ser Gly Asp Phe Ser Gln Ala His
50 55 60

Ser Thr Leu Lys Leu Ala Asn His Gln Arg Pro Val Ser Arg Gln Val
65 70 75 80

Thr Cys Leu Arg Thr Gln Val Leu Glu Asp Ser Glu Asp Ser Phe Cys
85 90 95

Arg Arg His Pro Gly Leu Gly Lys Ala Phe Pro Ser Gly Cys Ser Ala
100 105 110

Val Ser Glu Pro Ala Ser Glu Ser Val Val Gly Ala Leu Pro Ala Glu
115 120 125

His Gln Phe Ser Phe Met Glu Lys Arg Asn Gln Trp Leu Val Ser Gln
130 135 140

Leu Ser Ala Ala Ser Pro Asp Thr Gly His Asp Ser Asp Lys Ser Asp
145 150 155 160

Gln Ser Leu Pro Asn Ala Ser Ala Asp Ser Leu Gly Gly Ser Gln Glu
165 170 175

Met Val Gln Arg Pro Gln Pro His Arg Asn Arg Ala Gly Leu Asp Leu
180 185 190

Pro Thr Ile Asp Thr Gly Tyr Asp Ser Gln Pro Gln Asp Val Leu Gly
195 200 205

Ile Arg Gln Leu Glu Arg Pro Leu Pro Leu Thr Ser Val Cys Tyr Pro
210 215 220

Gln Asp Leu Pro Arg Pro Leu Arg Ser Arg Glu Phe Pro Gln Phe Glu
225 230 235 240

Pro Gln Arg Tyr Pro Ala Cys Ala Gln Met Leu Pro Pro Asn Leu Ser
245 250 255

Pro His Ala Pro Trp Asn Tyr His Tyr His Cys Pro Gly Ser Pro Asp
260 265 270

His Gln Val Pro Tyr Gly His Asp Tyr Pro Arg Ala Ala Tyr Gln Gln
275 280 285

Val Ile Gln Pro Ala Leu Pro Gly Gln Pro Leu Pro Gly Ala Ser Val
290 295 300

Arg Gly Leu His Pro Val Gln Lys Val Ile Leu Asn Tyr Pro Ser Pro
305 310 315 320

Trp Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Cys Ser Phe Pro Gly
325 330 335

Leu Pro Arg His Gln Asp Gln Pro His His Gln Pro Pro Asn Arg Ala
340 345 350

Gly Ala Pro Gly Glu Ser Leu Glu Cys Pro Ala Glu Leu Arg Pro Gln
355 360 365

Val Pro Gln Pro Pro Ser Pro Ala Ala Val Pro Arg Pro Pro Ser Asn
370 375 380

Pro Pro Ala Arg Gly Thr Leu Lys Thr Ser Asn Leu Pro Glu Glu Leu
385 390 395 400

Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val Val
405 410 415

Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile Asp
420 425 430

Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met Glu
435 440 445

Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser Pro

450

455

460

Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu Asp
 465 470 475 480

Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile Glu
 485 490 495

Phe Ile Lys Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu Phe
 500 505 510

Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr His
 515 520 525

Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu Leu
 530 535 540

Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr Leu
 545 550 555 560

Gln Val Val Pro Leu
 565

<210> 17
 <211> 1323
 <212> DNA
 <213> Mus musculus

<220>
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<400> 17
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 Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe
 1 5 10 15
 gaa ctt gag agg tat cca atg aac gcc cag ctg ctg ccg ccc cat cct 96
 Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro
 20 25 30
 tcc cca cag gcc cca tgg aac tgt cag tac tac tgc ccc gga ggg ccc 144
 Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
 35 40 45
 tac cac cac cag gtg cca cac ggc cat ggc tac cct cca gca gca gcc 192
 Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
 50 55 60
 tac cag caa gta ctc cag cct gct ctg cct ggg cag gtc ctt cct ggg 240
 Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
 65 70 75 80

gca agg gca aga ggc cca cgc cct gtg cag aag gtc atc ctg aat gac	288
Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp	
85 90 95	
tcc agc ccc caa gac caa gaa gag aga cct gca cag aga gac ttc tct	336
Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser	
100 105 110	
ttc ccg agg ctc ccg agg gac cag ctc tac cgc cca cca tct aat gga	384
Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly	
115 120 125	
gtg gaa gcc cct gag gag tcc ttg gac ctt cct gca gag ctg aga cca	432
Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro	
130 135 140	
cat ggt ccc cag gct cca tcc cta gct gcc gtg cct aga ccc cct agc	480
His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser	
145 150 155 160	
aac ccc tta gcc cga gga act cta aga acc agc aat ttg cca gaa gaa	528
Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu	
165 170 175	
tta cgg aaa gtc ttt atc act tat tct atg gac aca gcc atg gag gtg	576
Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val	
180 185 190	
gtg aaa ttt gtg aac ttt ctg ttg gtg aac ggc ttc caa act gcg att	624
Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile	
195 200 205	
gac ata ttt gag gat aga atc cgg ggt att gat atc att aaa tgg atg	672
Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met	
210 215 220	
gag cgc tat ctt cga gat aag aca gtg atg ata atc gta gca atc agc	720
Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser	
225 230 235 240	
ccc aaa tac aaa cag gat gtg gaa ggc gct gag tcg cag ctg gac gag	768
Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu	
245 250 255	
gac gag cat ggc tta cat act aag tac att cat cgg atg atg cag att	816
Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile	
260 265 270	
gag ttc ata agt cag gga agc atg aac ttc aga ttc atc cct gtg ctc	864
Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu	
275 280 285	
ttc cca aat gcc aag aag gag cat gtg ccg acc tgg ctt cag aac act	912
Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr	
290 295 300	
cat gtt tac agc tgg ccc aag aat aag aaa aac atc ctg ctg cgg ctg	960
His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu	
305 310 315 320	

ctc agg gag gaa gag tat gtg gct cct ccc cga ggc cct ctg ccc acc 1008
 Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr
 325 330 335

ctt cag gtg gta ccc ttg tgacgatggc cactccagct cagtgccage 1056
 Leu Gln Val Val Pro Leu
 340

ctgtttctcac agcattcttc tagcggagct ggctgggtggc acccaggccc tggaacacct 1116

cttctacaga gtcctctgtc tcttgagtct gagttgtcct cgctgggctt ccagagcttc 1176

agtgcctgga tgctgcaggt gacagaaaca aacatctatg accacaaaaa ctctcatcac 1236

ttcagctact tttatgagtc ggtcagatgc tctgtgtcct tagaccagtc taaatcatgc 1296

tcaaataata aaatgattat tctttgt 1323

<210> 18

<211> 342

<212> PRT

<213> Mus musculus

<400> 18

Gln Asp Leu Pro Gly Pro Leu Arg Ser Arg Glu Leu Pro Pro Gln Phe
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Glu Leu Glu Arg Tyr Pro Met Asn Ala Gln Leu Leu Pro Pro His Pro
 20 25 30

Ser Pro Gln Ala Pro Trp Asn Cys Gln Tyr Tyr Cys Pro Gly Gly Pro
 35 40 45

Tyr His His Gln Val Pro His Gly His Gly Tyr Pro Pro Ala Ala Ala
 50 55 60

Tyr Gln Gln Val Leu Gln Pro Ala Leu Pro Gly Gln Val Leu Pro Gly
 65 70 75 80

Ala Arg Ala Arg Gly Pro Arg Pro Val Gln Lys Val Ile Leu Asn Asp
 85 90 95

Ser Ser Pro Gln Asp Gln Glu Glu Arg Pro Ala Gln Arg Asp Phe Ser
 100 105 110

Phe Pro Arg Leu Pro Arg Asp Gln Leu Tyr Arg Pro Pro Ser Asn Gly
 115 120 125

Val Glu Ala Pro Glu Glu Ser Leu Asp Leu Pro Ala Glu Leu Arg Pro
 130 135 140

His Gly Pro Gln Ala Pro Ser Leu Ala Ala Val Pro Arg Pro Pro Ser
 145 150 155 160

Asn Pro Leu Ala Arg Gly Thr Leu Arg Thr Ser Asn Leu Pro Glu Glu
 165 170 175

Leu Arg Lys Val Phe Ile Thr Tyr Ser Met Asp Thr Ala Met Glu Val
 180 185 190

Val Lys Phe Val Asn Phe Leu Leu Val Asn Gly Phe Gln Thr Ala Ile
 195 200 205

Asp Ile Phe Glu Asp Arg Ile Arg Gly Ile Asp Ile Ile Lys Trp Met
 210 215 220

Glu Arg Tyr Leu Arg Asp Lys Thr Val Met Ile Ile Val Ala Ile Ser
 225 230 235 240

Pro Lys Tyr Lys Gln Asp Val Glu Gly Ala Glu Ser Gln Leu Asp Glu
 245 250 255

Asp Glu His Gly Leu His Thr Lys Tyr Ile His Arg Met Met Gln Ile
 260 265 270

Glu Phe Ile Ser Gln Gly Ser Met Asn Phe Arg Phe Ile Pro Val Leu
 275 280 285

Phe Pro Asn Ala Lys Lys Glu His Val Pro Thr Trp Leu Gln Asn Thr
 290 295 300

His Val Tyr Ser Trp Pro Lys Asn Lys Lys Asn Ile Leu Leu Arg Leu
 305 310 315 320

Leu Arg Glu Glu Glu Tyr Val Ala Pro Pro Arg Gly Pro Leu Pro Thr
 325 330 335

Leu Gln Val Val Pro Leu
 340

<210> 19
 <211> 207
 <212> PRT
 <213> Homo sapiens

<400> 19

Arg Lys Val Trp Ile Ile Tyr Ser Ala Asp His Pro Leu Tyr Val Asp

1	5	10	15
Val Val Leu Lys Phe Ala Gln Phe Leu Leu Thr Ala Cys Gly Thr Glu	20	25	30
Val Ala Leu Asp Leu Leu Glu Glu Gln Ala Ile Ser Glu Ala Gly Val	35	40	45
Met Thr Trp Val Gly Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser	50	55	60
Lys Ile Ile Val Leu Cys Ser Arg Gly Thr Arg Ala Lys Trp Gln Ala	65	70	75
Leu Leu Gly Arg Gly Ala Pro Val Arg Leu Arg Cys Asp His Gly Lys	85	90	95
Pro Val Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro Asp	100	105	110
Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe Ser	115	120	125
Glu Val Ser Cys Asp Gly Asp Val Pro Asp Leu Phe Gly Ala Ala Pro	130	135	140
Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile Gln	145	150	155
Asp Leu Glu Met Phe Gln Pro Gly Arg Met His Arg Val Gly Glu Leu	165	170	175
Ser Gly Asp Asn Tyr Leu Arg Ser Pro Gly Gly Arg Gln Leu Arg Ala	180	185	190
Ala Leu Asp Arg Phe Arg Asp Trp Gln Val Arg Cys Pro Asp Trp	195	200	205
<210> 20			
<211> 208			
<212> PRT			
<213> Mus musculus			
<400> 20			
Arg Lys Val Trp Ile Val Tyr Ser Ala Asp His Pro Leu Tyr Val Glu	1	5	10
			15

Val Val Leu Lys Phe Ala Gln Phe Leu Ile Thr Ala Cys Gly Thr Glu
20 25 30

Val Ala Leu Asp Leu Leu Glu Glu Gln Val Ile Ser Glu Val Gly Val
35 40 45

Met Thr Trp Val Ser Arg Gln Lys Gln Glu Met Val Glu Ser Asn Ser
50 55 60

Lys Ile Ile Ile Leu Cys Ser Arg Gly Thr Gln Ala Lys Trp Lys Ala
65 70 75 80

Ile Leu Gly Trp Ala Glu Pro Ala Val Gln Leu Arg Cys Asp His Trp
85 90 95

Lys Pro Ala Gly Asp Leu Phe Thr Ala Ala Met Asn Met Ile Leu Pro
100 105 110

Asp Phe Lys Arg Pro Ala Cys Phe Gly Thr Tyr Val Val Cys Tyr Phe
115 120 125

Ser Gly Ile Cys Ser Glu Arg Asp Val Pro Asp Leu Phe Asn Ile Thr
130 135 140

Ser Arg Tyr Pro Leu Met Asp Arg Phe Glu Glu Val Tyr Phe Arg Ile
145 150 155 160

Gln Asp Leu Glu Met Phe Glu Pro Gly Arg Met His His Val Arg Glu
165 170 175

Leu Thr Gly Asp Asn Tyr Leu Gln Ser Pro Ser Gly Arg Gln Leu Lys
180 185 190

Glu Ala Val Leu Arg Phe Gln Glu Trp Gln Thr Gln Cys Pro Asp Trp
195 200 205

<210> 21
<211> 190
<212> PRT
<213> Caenorhabditis elegans

<400> 21

Val Lys Val Met Ile Val Tyr Ala Asp Asp Asn Asp Leu His Thr Asp
1 5 10 15

Cys Val Lys Lys Leu Val Glu Asn Leu Arg Asn Cys Ala Ser Cys Asp

20

25

30

Pro Val Phe Asp Leu Glu Lys Leu Ile Thr Ala Glu Ile Val Pro Ser
35 40 45

Arg Trp Leu Val Asp Gln Ile Ser Ser Leu Lys Lys Phe Ile Ile Val
50 55 60

Val Ser Asp Cys Ala Glu Lys Ile Leu Asp Thr Glu Ala Ser Glu Thr
65 70 75 80

His Gln Leu Val Gln Ala Arg Pro Phe Ala Asp Leu Phe Gly Pro Ala
85 90 95

Met Glu Met Ile Ile Arg Asp Ala Thr His Asn Phe Pro Glu Ala Arg
100 105 110

Lys Lys Tyr Ala Val Val Arg Phe Asn Tyr Ser Pro His Val Pro Pro
115 120 125

Asn Leu Ala Ile Leu Asn Leu Pro Thr Phe Ile Pro Glu Gln Phe Ala
130 135 140

Gln Leu Thr Ala Phe Leu His Asn Val Glu His Thr Glu Arg Ala Asn
145 150 155 160

Val Thr Gln Asn Ile Ser Glu Ala Gln Ile His Glu Trp Asn Leu Cys
165 170 175

Ala Ser Arg Met Met Ser Phe Phe Val Arg Asn Pro Asn Trp
180 185 190

<210> 22

<211> 178

<212> PRT

<213> Caenorhabditis elegans

<400> 22

Phe Lys Val Met Leu Val Cys Pro Glu Val Ser Gly Arg Asp Glu Asp
1 5 10 15

Phe Met Met Arg Ile Ala Asp Ala Leu Lys Lys Ser Asn Asn Lys Val
20 25 30

Val Cys Asp Arg Trp Phe Glu Asp Ser Lys Asn Ala Glu Glu Asn Met
35 40 45

Leu His Trp Val Tyr Glu Gln Thr Lys Ile Ala Glu Lys Ile Ile Val
50 55 60

Phe His Ser Ala Tyr Tyr His Pro Arg Cys Gly Ile Tyr Asp Val Ile
65 70 75 80

Asn Asn Phe Phe Pro Cys Thr Asp Pro Arg Leu Ala His Ile Ala Leu
85 90 95

Thr Pro Glu Ala Gln Arg Ser Val Pro Lys Glu Val Glu Tyr Val Leu
100 105 110

Pro Arg Asp Gln Lys Leu Leu Glu Asp Ala Phe Asp Ile Thr Ile Ala
115 120 125

Asp Pro Leu Val Ile Asp Ile Pro Ile Glu Asp Val Ala Ile Pro Glu
130 135 140

Asn Val Pro Ile His His Glu Ser Cys Asp Ser Ile Asp Ser Arg Asn
145 150 155 160

Asn Ser Lys Thr His Ser Thr Asp Ser Gly Val Ser Ser Leu Ser Ser
165 170 175

Asn Ser

<210> 23
<211> 1107
<212> DNA
<213> Homo sapiens

<400> 23
gtgtggcctc aggtataaga gcggtgctg ccaggtgcat ggccaggtgc acctgtggga 60
ttgccgccag gtgtgcaggc cgctccaagc ccagcctgcc ccgctgccgc caccatgacg 120
ctctctcccc gctctctgtt tctgacctgg ctgcacacat gctgggcca ccatgacccc 180
tccctcaggg ggcacccccca cagtcacggt accccacact gctactcggc tgaggaactg 240
cccctcggcc agggcccccc acacctgctg gctcgaggtg ccaagtgggg gcaggctttg 300
cctgtagccc tgggtgtccag cctggaggca gcaagccaca gggggaggca cgagaggccc 360
tcagctacga cccagtgcgc ggtgctgcgg ccggaggagg tgttgagggc agacaccac 420
cagcgtcca tctcacctg gagataccgt gtggacacgg atgaggaccg ctatccacag 480
aagctggcct tcgccgagtg cctgtgcaga ggctgtatcg atgcacggac gggccgcgag 540

acagctgcgc tcaactccgt ggggtgctc cagagcctgc tgggtgctgcg ccgccggccc 600
 tgctcccgcg acggctcggg gctccccaca cctggggcct ttgccttcca caccgagttc 660
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Leu Ala His His Asp Pro Ser Leu Arg Gly His Pro His Ser His Gly
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Thr Pro His Cys Tyr Ser Ala Glu Glu Leu Pro Leu Gly Gln Ala Pro
 35 40 45

Pro His Leu Leu Ala Arg Gly Ala Lys Trp Gly Gln Ala Leu Pro Val
 50 55 60

Ala Leu Val Ser Ser Leu Glu Ala Ala Ser His Arg Gly Arg His Glu
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Arg Pro Ser Ala Thr Thr Gln Cys Pro Val Leu Arg Pro Glu Glu Val
 85 90 95

Leu Glu Ala Asp Thr His Gln Arg Ser Ile Ser Pro Trp Arg Tyr Arg
 100 105 110

Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe Ala Glu
 115 120 125

Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu Thr Ala

130

135

140

Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu Arg Arg
145 150 155 160

Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly Ala Phe
165 170 175

Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr Cys Val
180 185 190

Leu Pro Arg Ser Val
195